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RAW SEQUENCE LISTING DATE: 07/10/2002  
 PATENT APPLICATION: US/09/989,025A TIME: 10:47:24

Input Set : A:\PTO.PG.txt  
 Output Set: N:\CRF3\07102002\I989025A.raw

3 <110> APPLICANT: NAKAI, JUNICHI  
 5 <120> TITLE OF INVENTION: METHOD FOR PRODUCING A BIOSENSOR PROTEIN CAPABLE OF  
 REGULATING A  
 6 FLUORESCENCE PROPERTY OF GREEN FLUORESCENT PROTEIN, AND THE BIOSENSOR PROTEIN  
 7 PRODUCED BY THE METHOD  
 9 <130> FILE REFERENCE: 216339US0  
 11 <140> CURRENT APPLICATION NUMBER: 09/989,025A  
 12 <141> CURRENT FILING DATE: 2001-11-21  
 14 <150> PRIOR APPLICATION NUMBER: JP/2000-356047  
 15 <151> PRIOR FILING DATE: 2000-11-22  
 17 <160> NUMBER OF SEQ ID NOS: 17  
 19 <170> SOFTWARE: PatentIn version 3.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 717  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Aequorea victoria  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1)..(717)  
 29 <223> OTHER INFORMATION:  
 32 <400> SEQUENCE: 1  
 33 atg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48  
 34 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 35 1 5 10 15  
 37 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96  
 38 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 39 20 25 30  
 41 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144  
 42 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 43 35 40 45  
 45 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192  
 46 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 47 50 55 60  
 49 acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag 240  
 50 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 51 65 70 75 80  
 53 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288  
 54 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 55 85 90 95  
 57 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336  
 58 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 59 100 105 110  
 61 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384  
 62 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

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63          115          120          125
65 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
66 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
67          130          135          140
69 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
70 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
71 145          150          155          160
73 atc aag gtg aac ttc aag atc cgc cac aac atc gag gag ggc agc gtg      528
74 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
75          165          170          175
77 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc      576
78 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
79          180          185          190
81 gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc      624
82 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
83          195          200          205
85 aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg      672
86 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
87          210          215          220
89 acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa      717
90 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
91 225          230          235
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95 <211> LENGTH: 238
96 <212> TYPE: PRT
97 <213> ORGANISM: Aequorea victoria
99 <400> SEQUENCE: 2
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105 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
106          20          25          30
109 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
110          35          40          45
113 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
114          50          55          60
117 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
118 65          70          75          80
121 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
122          85          90          95
125 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
126          100          105          110
129 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
130          115          120          125
133 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
134          130          135          140
137 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
138 145          150          155          160
141 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
142          165          170          175

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145 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
146           180           185           190
149 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
150           195           200           205
153 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
154           210           215           220
157 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
158 225           230           235
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 447
163 <212> TYPE: DNA
164 <213> ORGANISM: Rattus norvegicus
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(444)
169 <223> OTHER INFORMATION:
172 <400> SEQUENCE: 3
173 gct gac caa ctg act gaa gag cag atc gca gaa ttc aaa gaa gct ttc      48
174 Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe
175 1           5           10           15
177 tcc cta ttt gac aag gac ggg gat ggg aca ata aca acc aag gag ctg      96
178 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
179           20           25           30
181 ggg acg gtg atg cgg tct ctg ggg cag aac ccc aca gaa gca gag ctg      144
182 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
183           35           40           45
185 cag gac atg atc aat gaa gta gat gcc gac ggt aat ggc aca atc gac      192
186 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
187           50           55           60
189 ttc cct gaa ttc ctg aca atg atg gca aga aaa atg aaa gac aca gac      240
190 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
191 65           70           75           80
193 agt gaa gaa gaa att aga gaa gcg ttc cgt gtg ttt gat aag gat ggc      288
194 Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
195           85           90           95
197 aat ggc tac atc agt gca gca gag ctt cgc cac gtg atg aca aac ctt      336
198 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
199           100          105          110
201 gga gag aag tta aca gat gaa gag gtt gat gaa atg atc agg gaa gca      384
202 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
203           115          120          125
205 gac atc gat ggg gat ggt cag gta aac tac gaa gag ttt gta caa atg      432
206 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
207           130          135          140
209 atg aca gcg aag tga      447
210 Met Thr Ala Lys
211 145
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 148

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216 <212> TYPE: PRT
217 <213> ORGANISM: Rattus norvegicus
219 <400> SEQUENCE: 4
221 Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe
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225 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
226          20          25          30
229 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
230          35          40          45
233 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
234          50          55          60
237 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
238 65          70          75          80
241 Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
242          85          90          95
245 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
246          100         105         110
249 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
250          115         120         125
253 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
254          130         135         140
257 Met Thr Ala Lys
258 145
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262 <211> LENGTH: 63
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Synthetic DNA
269 <220> FEATURE:
270 <221> NAME/KEY: CDS
271 <222> LOCATION: (1)..(63)
272 <223> OTHER INFORMATION:
275 <400> SEQUENCE: 5
276 tca tca cgt cgt aag tgg aat aag aca ggt cac gca gtc aga gct ata      48
277 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
278 1          5          10          15
280 ggt cgg ctg agc tca      63
281 Gly Arg Leu Ser Ser
282          20
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286 <211> LENGTH: 21
287 <212> TYPE: PRT
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Synthetic DNA
293 <400> SEQUENCE: 6
295 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
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299 Gly Arg Leu Ser Ser
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306 <213> ORGANISM: Artificial Sequence
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309 <223> OTHER INFORMATION: Synthetic DNA
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (1)..(1248)
314 <223> OTHER INFORMATION:
317 <400> SEQUENCE: 7
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320 1          5          10          15
322 aga gct ata ggt cgg ctg agc tca ctc gag aac gtc tat atc atg gcc      96
323 Arg Ala Ile Gly Arg Leu Ser Ser Leu Glu Asn Val Tyr Ile Met Ala
324          20          25          30
326 gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac      144
327 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
328          35          40          45
330 atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc      192
331 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
332          50          55          60
334 ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc      240
335 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
336 65          70          75          80
338 acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg      288
339 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
340          85          90          95
342 gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac      336
343 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
344          100          105          110
346 gag ctg tac aag ggc ggt acc gga ggg agc atg gtg agc aag ggc gag      384
347 Glu Leu Tyr Lys Gly Gly Thr Gly Gly Ser Met Val Ser Lys Gly Glu
348          115          120          125
350 gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac      432
351 Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
352          130          135          140
354 gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc      480
355 Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
356 145          150          155          160
358 acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg      528
359 Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
360          165          170          175
362 ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag      576
363 Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln
364          180          185          190

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**VERIFICATION SUMMARY**

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